

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/973,815DATE: 06/21/1999  
TIME: 14:24:53

INPUT SET: S32263.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT:  
6 (A) NAME: Deutsches Krebsforschungszentrum Stiftung des  
7 ffentlichen Rechts  
8 (B) STREET: Im Neuenheimer Feld 280  
9 (C) CITY: Heidelberg  
10 (E) COUNTRY: Germany  
11 (F) POSTAL CODE: 69120  
12  
13 (ii) TITLE OF INVENTION: DNase active Protein  
14  
15 (iii) NUMBER OF SEQUENCES: 3  
16  
17 (v) COMPUTER-READABLE FORM:  
18 (A) MEDIUM TYPE: Floppy disk  
19 (B) COMPUTER: IBM PC compatible  
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
21 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)  
22  
23 (vi) CURRENT APPLICATION DATA:  
24 (A) APPLICATION NUMBER:  
25 (B) FILING DATE:  
26  
27 (vii) PRIOR APPLICATION DATA:  
28 (A) APPLICATION NUMBER: PCT/DE96/01016  
29 (B) FILING DATE:  
30  
31 (A) APPLICATION NUMBER: DE 195 21 046.8  
32 (B) FILING DATE: 09-JUN-1995  
33  
34  
35 (2) INFORMATION FOR SEQ ID NO: 1:  
36  
37 (i) SEQUENCE CHARACTERISTICS:  
38 (A) LENGTH: 2661 Base pairs  
39 (B) TYPE: Nucleotide  
40 (C) STRANDEDNESS: double  
41 (D) TOPOLOGY: linear  
42  
43 (ii) MOLECULE TYPE: cDNA  
44  
45  
46 (ix) FEATURE:

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47      (A) NAME/KEY: CDS
48      (B) LOCATION: 795..1700
49
50
51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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53      CTTGAACGCC TGACCTCGTA TCCACCCGCC TCAGCCTCCC AAAGTGCTGG GATTACAGGC      60
54
55      ATGAGCCACC ACGCCCAGCC CATAATTTAT TGATTTTTTA AAATTTGTCC AGCCTTCTAT      120
56
57      TACCACGTCG AATCCATTAG CTACAGCCAT CCCATGAGAA GCTGAGTGGG TTCAGCCCCA      180
58
59      CCTCCTGCTC ACAGACCCTG TCCGAGCACC TCATTTGTCC CAACAGCATT ACTGCAGGAC      240
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61      CCCCAGGACG TTGGACTGCC AGCTCCCTGG GTCTCCTCCT CTCTGGGGCA GATCCTCAGT      300
62
63      CCTCCCTTGA CTTACAGACT GTGGCCAGAT CATGTGTGGA CTGTCCCTCT CTTTGGGTCT      360
64
65      CCAGAGCGCT TGCATCAAAC ACCCCTAACT CAGAAGTGTG CAGCCACACT GGGACTCAGA      420
66
67      ACCCAACAAC AGGGACAGAA GACTCACGCC CTTGGGGTGC CCGGTCTCGT GGCATCAGGC      480
68
69      ATGACTTCCA GCTCCTGCGC CTTCCCCAGC AACTGCTGAC TGGGGACCCA GACCGGGAGC      540
70
71      TGAGCGACGG GCCTGGCGAG CGAAGCTCGG GGTCTCACTC AGGCACCAGC CCCTCCTTGC      600
72
73      CCCAGGCTTG AGTGA CTCAC AGCCCTATTC AGGCAGGAGC TGCTCTTCTG GGGTATCGCG      660
74
75      ATCCACTTAA GGATGAGGCA GACTTGGTGA CAAGCTGGTC TGAGCAGCGC TTCCAGAGCC      720
76
77      AGAACTGAGC CCAGTGAGAG CGCACCCCTGG AGCAGCCTGG ATTCCTGGGG TGTCCCCGGC      780
78
79      AGCCACACAC AGCC ATG CAC TAC CCA ACT GCA CTC CTC TTC CTC ATC CTG      830
80      Met His Tyr Pro Thr Ala Leu Leu Phe Leu Ile Leu
81      1 5 10
82
83      GCC AAT GGG GCC CAG GCC TTT CGC ATC TGC GCC TTC AAT GCC CAG CGG      878
84      Ala Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala Gln Arg
85      15 20 25
86
87      CTG ACA CTG GCC AAG GTG GCC AGG GAG CAG GTG ATG GAC ACC TTA GTT      926
88      Leu Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr Leu Val
89      30 35 40
90
91      CGG ATA CTG GCT CGC TGT GAC ATC ATG GTG CTG CAG GAG GTG GTA GAC      974
92      Arg Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp
93      45 50 55 60
94
95      TCT TCC GGC AGC GCC ATC CCC CTC CTG CTT CGA GAA CTC AAT CGA TTT      1022
96      Ser Ser Gly Ser Ala Ile Pro Leu Leu Leu Arg Glu Leu Asn Arg Phe
97      65 70 75
98
99      GAT GGC TCT GGG CCC TAC AGC ACC CTG AGC AGC CCC CAG CTG GGG CGC      1070

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100	Asp Gly Ser Gly Pro Tyr Ser Thr Leu Ser Ser Pro Gln Leu Gly Arg	
101	80 85 90	
102		
103	AGC ACC TAC ATG GAG ACG TAT GTG TAC TTC TAT CGG TCA CAC AAA ACA	1118
104	Ser Thr Tyr Met Glu Thr Tyr Val Tyr Phe Tyr Arg Ser His Lys Thr	
105	95 100 105	
106		
107	CAG GTC CTG AGT TCC TAC GTG TAC AAC GAT GAG GAT GAC GTC TTT GCC	1166
108	Gln Val Leu Ser Ser Tyr Val Tyr Asn Asp Glu Asp Asp Val Phe Ala	
109	110 115 120	
110		
111	CGG GAG CCA TTT GTG GCC CAG TTC TCT TTG CCC AGC AAT GTC CTT CCC	1214
112	Arg Glu Pro Phe Val Ala Gln Phe Ser Leu Pro Ser Asn Val Leu Pro	
113	125 130 135 140	
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115	AGC CTG GTG TTG GTC CCG CTG CAC ACC ACT CCT AAG GCC GTA GAG AAG	1262
116	Ser Leu Val Leu Val Pro Leu His Thr Thr Pro Lys Ala Val Glu Lys	
117	145 150 155	
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119	GAG CTG AAC GCC CTC TAC GAT GTG TTT CTG GAG GTC TCC CAG CAC TGG	1310
120	Glu Leu Asn Ala Leu Tyr Asp Val Phe Leu Glu Val Ser Gln His Trp	
121	160 165 170	
122		
123	CAG AGC AAG GAC GTG ATC CTG CTT GGG GAC TTC AAT GCT GAC TGC GCT	1358
124	Gln Ser Lys Asp Val Ile Leu Leu Gly Asp Phe Asn Ala Asp Cys Ala	
125	175 180 185	
126		
127	TCA CTG ACC AAA AAG CGC CTG GAC AAG CTG GAG CTG CGG ACT GAG CCA	1406
128	Ser Leu Thr Lys Lys Arg Leu Asp Lys Leu Glu Leu Arg Thr Glu Pro	
129	190 195 200	
130		
131	GGC TTC CAC TGG GTG ATT GCC GAT GGG GAG GAC ACC ACA GTG CGG GCC	1454
132	Gly Phe His Trp Val Ile Ala Asp Gly Glu Asp Thr Thr Val Arg Ala	
133	205 210 215 220	
134		
135	AGC ACC CAC TGC ACC TAT GAC CGC GTC GTG CTG CAC GGG GAG CGC TGC	1502
136	Ser Thr His Cys Thr Tyr Asp Arg Val Val Leu His Gly Glu Arg Cys	
137	225 230 235	
138		
139	CGG AGT CTG CTG CAC ACT GCG GCT GCC TTT GAC TTC CCC ACG AGC TTC	1550
140	Arg Ser Leu Leu His Thr Ala Ala Phe Asp Phe Pro Thr Ser Phe	
141	240 245 250	
142		
143	CAG CTC ACC GAG GAG GAG GCC CTC AAC ATC AGT GAC CAC TAC CCC GTG	1598
144	Gln Leu Thr Glu Glu Glu Ala Leu Asn Ile Ser Asp His Tyr Pro Val	
145	255 260 265	
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147	GAG GTG GAG CTG AAG CTG AGC CAG GCG CAC AGC GTC CAG CCT CTC AGC	1646
148	Glu Val Glu Leu Lys Leu Ser Gln Ala His Ser Val Gln Pro Leu Ser	
149	270 275 280	
150		
151	CTC ACT GTT CTG TTG CTG CTA TCA CTC CTG TCC CCT CAG CTG TGC CCT	1694
152	Leu Thr Val Leu Leu Leu Leu Ser Leu Leu Ser Pro Gln Leu Cys Pro	

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153					
154					
155	GCT GCC TGAGCGTCCC CCTACCCCCC CAGGGCCTGC TGCCTTTTGG GACTTAAACC				1750
156	Ala Ala				
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158					
159	CCAGCCTCCC CCGTCCATCC AGCCCTGGGG CTGGGGGGCT TCAACTATAG TTGCCCTGTG				1810
160					
161	ACTGTAGTCC ACCCCTGCCT GCCTTGTTTG ATTTGGCTCT TGTTCCTTGG TTGGGCTTGT				1870
162					
163	GCCTAGATTA GGAGAGGAAG CCAGGGGCCC TGCACATCATG CCACCTGCCA GGTAGTGTAG				1930
164					
165	TATCAGGAGT GGAGACAAAG TGGGCTCTGG GTTGGGGTAG GGGAAGGGAG GGTTCAGAAA				1990
166					
167	GAGGAATGAA GATGTTGTAT GACAAGAAGG AAAGTTACTG AGAACAAAAA CCCAGATTGG				2050
168					
169	TGAGATAGGA CACTTGTGCA GCAGATATGC CAATGGGCCA TGTTTATTGT GGATGGGTAA				2110
170					
171	GAATCACCAG GAAACCATTA AGCCCCAATA GCTACAAGGA GGGTGGTTAA TCTGCTATAT				2170
172					
173	CAAACTCCTT CCCTGAAACC AGCAAACACC GGGAAACATT TTGGCTCATT ATAATCCGGT				2230
174					
175	GAACAATGCA GTCAGGCCTG TTATAACCGC TGAGCAGCCA CACTCGCACC TCCTGGGTGC				2290
176					
177	TGTAGTCTGT GTTGGTACAG GCTTCTGCAT GCCTGGTAAA GTCCAGCCAA GGCTGGTCAA				2350
178					
179	GGCAACATCT CCACACAGAA AATCTGCACC AGTTATGTAA GCTAAAAAGC TGTGTGAACC				2410
180					
181	CAGGTGTCCC GGAAAGGGGC TGCAGGACAC AGCAAAATGC CAGCAGCGTG CCGGACCCCT				2470
182					
183	CCCTTCCATC CTCCTCTCCA AAGAACAGAG GTCAGGAAAA AACTGGCTG GGACGCTAGA				2530
184					
185	AGGGTCATGT GTTAACTATA ATCACATTTA TGGTTTGGAA CCATCACCCC AAGGTAAAAA				2590
186					
187	AAAAAATAAA AGGTATGTTT GGCAAAATAA AATAAAGGTA ATTAAAAACC TAAAAAATAA				2650
188					
189	AAAAAAAAAA A				2661

190  
191

192 (2) INFORMATION FOR SEQ ID NO: 2:

193

194 (i) SEQUENCE CHARACTERISTICS:

195 (A) LENGTH: 43 Base pairs

196 (B) TYPE: Nucleotide

197 (C) STRANDEDNESS: single

198 (D) TOPOLOGY: linear

199

200 (ii) MOLECULE TYPE: other nucleic acid

201 (A) DESCRIPTION: /desc = "DNA-Primer"

202

203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

204

205 CAGGGATCCG ATGACGATGA CAAAATGCAC TACCCAACTG CAC

43

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206  
207  
208 (2) INFORMATION FOR SEQ ID NO: 3:  
209  
210 (i) SEQUENCE CHARACTERISTICS:  
211 (A) LENGTH: 27 Base pairs  
212 (B) TYPE: Nucleotide  
213 (C) STRANDEDNESS: single  
214 (D) TOPOLOGY: linear  
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216 (ii) MOLECULE TYPE: other nucleic acid  
217 (A) DESCRIPTION: /desc = "DNA-Primer"  
218  
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
220  
221 GGGGGATCCT CAGGCAGCAG GGCACAG  
222

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/973,815**DATE: 06/21/1999  
TIME: 14:24:55**INPUT SET: S32263.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Deutsches Krebsforschungszentrum Stiftung de
8	Unknown or Misplaced Identifier	(B) STREET: Im Neuenheimer Feld 280
9	Unknown or Misplaced Identifier	(C) CITY: Heidelberg
10	Unknown or Misplaced Identifier	(E) COUNTRY: Germany
11	Unknown or Misplaced Identifier	(F) POSTAL CODE: 69120